

&lt;!--StartFragment--&gt;RESULT 1

ADC00348

ID ADC00348 standard; protein; 441 AA.

APPENDIX B SEQ ID NO; 24

XX

AC ADC00348;

XX

DT 15-JUN-2007 (revised)

DT 04-DEC-2003 (first entry)

XX

DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 393.

XX

KW enterohaemorrhagic; anti-bacterial; BOND\_PC; hypothetical protein;

KW hypothetical protein ECs1812 [Escherichia coli 0157:H7];

KW hypothetical protein ECs1812 [Escherichia coli 0157:H7 str. Sakai];

KW unknown protein encoded by cryptic prophage CP-933P;

KW hypothetical protein [Escherichia coli 0157:H7 str. Sakai].

XX

OS Escherichia coli; 0157:H7.

XX

PN JP2002355074-A.

XX

PD 10-DEC-2002.

XX

PF 24-JAN-2002; 2002JP-00015959.

XX

PR 24-JAN-2001; 2001JP-00112010.

XX

PA (UYTS-) UNIV TSUKUBA.

XX

DR WPI; 2003-451640/43.

DR PC:NCBI; gil3259568.

XX

PT Enterohemorrhagic Escherichia coli 0157:H7-specific nucleic acid molecule

PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

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PS Claim 3; SEQ ID NO 393; 2067pp; Japanese.

XX

CC The invention relates to a novel enterohaemorrhagic Escherichia coli

CC 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention

CC has anti-bacterial activity. The polypeptide can be used in detection

CC and/or treatment of 0157:H7 infection. The nucleotide sequence of the

CC genome of Enterohaemorrhagic E coli 0157:H7 was determined. The present

CC sequence represents an E. coli 0157:H7-specific polypeptide of the

CC invention.

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed

CC information from BOND.

XX

SQ Sequence 441 AA;

Query Match 100.0%; Score 2341; DB 6; Length 441;

Best Local Similarity 100.0%; Pred. No. 1.1e-197;

Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVFNIPDDIQQHAPECGET	60
Db	1	MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVFNIPDDIQQHAPECGET	60
Qy	61	TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY	120
Db	61	TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY	120
Qy	121	GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST	180
Db	121	GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST	180
Qy	181	GTSATTSTVTTEPKDPIPWFLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY	240

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      |||
Db      181 GTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGGETPLTPDGPKANY 240
      |||
Qy      241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNPNNTKYAVLTNAAANALGALGGF 300
      |||
Db      241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNPNNTKYAVLTNAAANALGALGGF 300
      |||
Qy      301 AVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPLKPDITLWWAGATLGAADLNKAEFEV 360
      |||
Db      301 AVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPLKPDITLWWAGATLGAADLNKAEFEV 360
      |||
Qy      361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
      |||
Db      361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
      |||
Qy      421 LPHHNPSNHVDIFDIIQETRV 441
      |||
Db      421 LPHHNPSNHVDIFDIIQETRV 441
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